

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/550,985

Source: TFWP

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RAW SEQUENCE LISTING

DATE: 06/21/2006

PATENT APPLICATION: US/10/550,985

TIME: 10:35:49

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4     EULENBERG, KARSTEN
5     NGUYEN, TRI
6     BURK, ULRIKE
8 <120> TITLE OF INVENTION: USE OF A SECRETED PROTEIN FOR PREVENTING AND TREATING
9     OBESITY, DIABETES AND/OR METABOLIC SYNDROME
11 <130> FILE REFERENCE: 18744-0033
13 <140> CURRENT APPLICATION NUMBER: 10/550,985
14 <141> CURRENT FILING DATE: 2005-09-26
16 <150> PRIOR APPLICATION NUMBER: PCT/EP04/003244
17 <151> PRIOR FILING DATE: 2004-03-26
19 <150> PRIOR APPLICATION NUMBER: EP 03006948.8
20 <151> PRIOR FILING DATE: 2003-03-26
22 <160> NUMBER OF SEQ ID NOS: 7
24 <170> SOFTWARE: PatentIn Ver. 3.3
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 2767
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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34 gctcggcagt gtggtgccag aatgtgaaga cggcgtccga ctgcggggca gtgaagcact 180
35 gcctgcagac cgtttggaac aagccaacag tgaaatccct tccctgcgac atatgcaaag 240
36 acgtttgtcac cgcagctggg gatatgctga aggacaatgc cactgaggag gagatccttg 300
37 tttacttgga gaagacctgt gactggcttc cgaaaccgaa catgtctgct tcatgcaagg 360
38 agatagtgga ctctacctc cctgtcatcc tggacatcat taaaggagaa atgagccgtc 420
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43 tccagactgc tgtacggacc aactccacct ttgtccaggc cttggtggaa catgtcaagg 720
44 aggagtgtga ccgcctgggc cctggcatgg ccgacatatg caagaactat atcagccagt 780
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47 cctccaagaa tgtcatccct gccctggaac tgggtggagcc cattaagaag cacgaggtcc 960
48 cagcaaagtc tgatgtttac tgtgaggtgt gtgaattcct ggtgaaggag gtgaccaagc 1020
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53 tctgcgaagt gtgcaagaag ctggtggggt atttggatcg caacctggag aaaaacagca 1320
54 ccaagcagga gatcctggct gctcttgaga aaggctgcag cttcctgcca gaccttacc 1380

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56 aggtgatgga tccttccttc gtgtgcttga aaattggagc ctgcccctcg gcccataagc 1500
57 ccttgttggg aactgagaag tgtatatggg gcccagcta ctggtgccag aacacagaga 1560
58 cagcagccca gtgcaatgct gtcgagcatt gcaaacgcca tgtgtggaac taggaggagg 1620
59 aatattccat cttggcagaa accacagcat tgggtttttt ctacttgtgt gtctggggga 1680
60 atgaacgcac agatctgttt gactttgtta taaaaatagg gctccccac ctccccatt 1740
61 tctgtgtcct ttattgtagc attgctgtct gcaagggagc ccctagcccc tagcccctgg 1800
62 cagacatagc tgcttcagtg ccccttttct ctctgctaga tggatgttga tgcactggag 1860
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68 atagcatagg gattttggaa gcagctgctg gtgcttggg acatcagtg ggccaaggg 2220
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72 ctgctcgtgt tgctacatg tccctggctg ttgaggcgt gcttcagcct gcacccctcc 2460
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76 cttctggttg ccaggagaca gcaagcaaag ccagcaggac atgaagttgc tattaaatgg 2700
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81 <210> SEQ ID NO: 2

82 <211> LENGTH: 524

83 <212> TYPE: PRT

84 <213> ORGANISM: Homo sapiens

86 <400> SEQUENCE: 2

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90 Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp
91 20 25 30
93 Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys
94 35 40 45
96 Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp
97 50 55 60
99 Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn
100 65 70 75 80
102 Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp
103 85 90 95
105 Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser
106 100 105 110
108 Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro
109 115 120 125
111 Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His
112 130 135 140
114 Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro
115 145 150 155 160

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117 Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro
118                               165                               170                               175
120 Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys
121                               180                               185                               190
123 Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile
124                               195                               200                               205
126 Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu
127                               210                               215                               220
129 His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile
130 225                               230                               235                               240
132 Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met
133                               245                               250                               255
135 Met His Met Gln Pro Lys Glu Ile Cys Ala Leu Val Gly Phe Cys Asp
136                               260                               265                               270
138 Glu Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala Lys Val Ala
139                               275                               280                               285
141 Ser Lys Asn Val Ile Pro Ala Leu Glu Leu Val Glu Pro Ile Lys Lys
142                               290                               295                               300
144 His Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys Glu Phe
145 305                               310                               315                               320
147 Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys
148                               325                               330                               335
150 Glu Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro Lys Ser
151                               340                               345                               350
153 Leu Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly Ser Ser Ile
154                               355                               360                               365
156 Leu Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys Ser Met
157                               370                               375                               380
159 Leu His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val His Val
160 385                               390                               395                               400
162 Thr Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val
163                               405                               410                               415
165 Gly Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile
166                               420                               425                               430
168 Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln
169                               435                               440                               445
171 Lys Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu
172                               450                               455                               460
174 Ile Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys Ile Gly
175 465                               470                               475                               480
177 Ala Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys Cys Ile
178                               485                               490                               495
180 Trp Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala Ala Gln Cys
181                               500                               505                               510
183 Asn Ala Val Glu His Cys Lys Arg His Val Trp Asn
184                               515                               520
187 <210> SEQ ID NO: 3
188 <211> LENGTH: 1146
189 <212> TYPE: DNA

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190 <213> ORGANISM: Homo sapiens
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195 caaagcctgg agcaagcatt gcagtgcaga gccctagggc attgcctaca ggaagtctgg 180
196 ggacatgtgg gagccgatga cctatgccaa gagtgtgagg acatcgcca catccttaac 240
197 aagatggcca aggaggccat tttccaggac acgatgagga agttcctgga gcaggagtgc 300
198 aacgtcctcc ccttgaagct gctcatgccc cagtgcacc aagtgttga cgactacttc 360
199 cccctgggtca tcgactactt ccagaaccag attgactcaa acggcatctg tatgcacctg 420
200 ggctgtgca aatcccggca gccagagcca gagcaggagc cagggatgtc agaccccctg 480
201 cccaaacctc tgcgggaccc tctgccagac cctctgctgg acaagctcgt cctccctgtg 540
202 ctgcccgggg cctccaggc gaggcctggg cctcacacac aggatctctc cgagcagcaa 600
203 ttccccattc ctctccccta ttgctggctc tgcagggtc tgatcaagcg gatccaagcc 660
204 atgattccca aggggtgcgt acgtgtggca gtggcccagg tgtgccgctt ggtacctctg 720
205 gtggcgggcg gcatctgcca gtgctgggtc gagcgctact ccgtcatcct gctcgacacg 780
206 ctgctggggc gcatgtgtcc ccagctgggtc tgccgcctcg tcctccggtg ctccatggat 840
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208 ctctgcatgt ccgtgaccac ccaggccggg aacagcagcg agcaggccat accacaggca 960
209 atgctccagg cctgtgttgg ctcttggtg gacagggaaa agtgcaagca atttgtggag 1020
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212 ctttga 1146
215 <210> SEQ ID NO: 4
216 <211> LENGTH: 381
217 <212> TYPE: PRT
218 <213> ORGANISM: Homo sapiens
220 <400> SEQUENCE: 4
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222 1 5 10 15
224 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
225 20 25 30
227 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
228 35 40 45
230 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
231 50 55 60
233 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
234 65 70 75 80
236 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
237 85 90 95
239 Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
240 100 105 110
242 Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
243 115 120 125
245 Asn Gln Ile Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys
246 130 135 140
248 Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
249 145 150 155 160
251 Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
252 165 170 175

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254 Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
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257 Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
258          195          200          205
260 Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
261          210          215          220
263 Gly Ala Leu Arg Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
264 225          230          235          240
266 Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
267          245          250          255
269 Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
270          260          265          270
272 Leu Val Leu Arg Cys Ser Met Asp Ser Ala Gly Pro Arg Ser Pro
273          275          280          285
275 Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser
276          290          295          300
278 Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala
279 305          310          315          320
281 Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys
282          325          330          335
284 Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg
285          340          345          350
287 Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr
288          355          360          365
290 Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu
291          370          375          380
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295 <211> LENGTH: 1521
296 <212> TYPE: DNA
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299 <400> SEQUENCE: 5
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302 gtggcaggcc cccaccttct tgcacacagc cacggggtcc atcatgtcct tgagactctc 180
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313 ctctctgcag agctcctgcg gggggagaag cctcagtgtc tggtcagcag ggacaaaaaa 840
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315 ctggatgttc aagtcggcca aggtcaagtt ggaccggaca gcctcctgga gtcgggagac 960
316 ctgccgtaca cagtcttggc acagagctcc ttcaggcgcc tggcgggggt ggaaggtaag 1020
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